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(54) Title: DIAGNOSTIC METHOD FOR ALZHEIMER'S DISEASE

(57) Abstract

The present invention is directed to methods and kits for diagnosing, subtyping and monitoring Alzheimer's disease. The invention is based, in part, on the discovery that proteolytic fragments of the amino and carboxy terminal amino acid residues of *tau*-proteins are released from the neurofibrillary tangles associated with the disease and can be detected in body fluids outside the brain. The *tau*-proteins will be purified or chemically synthesized and peptide fragments of the amino terminal and carboxy terminal regions will be obtained proteolytically or synthesized chemically and will be used in generating *tau* specific antibodies for use in diagnostic kits for the detection of Alzheimer's disease. These diagnostic kits will be used in screening the body fluids of individuals for the presence of *tau*-peptide fragments. Alternatively, the *tau*-peptides themselves may be used in diagnostic kits for screening the body fluids of individuals for the presence of circulating autoantibodies.

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& Meyer, 1979, *Medical Neurology*, pp. 175-179 MacMillan Publishing Co.). Alzheimer's disease afflicts an estimated 4 million human beings in the United States alone at a cost of 35 billion dollars a year (Hay & Ernst, 1987, *Am. J. Public Health*, 77:1169-1175). It is found in 10% of the population over the age of 65 and 47% of the population over the age of 85 (Evans et al., 1989, *JAMA*, 262:2551-2556). In addition, the disease is found at much lower levels in the younger age groups, usually beginning at about 30 years of age and even rarely in late childhood (Adams & Victor, 1977, *Principles of Neurology*, pp. 401-407).

The etiology of Alzheimer's disease is unknown. Evidence for a genetic contribution comes from several important observations such as the familial incidence, pedigree analysis, monozygotic and dizygotic twin studies and the association of the disease with Down's syndrome (for review see Baraitser, 1990, *The Genetics of Neurological Disorders*, 2nd edition, pp. 85-88). Nevertheless, this evidence is far from definitive and it is clear that one or more other factors are also required. Elevated concentrations of aluminum have been found in the brains of some patients dying with Alzheimer's disease (Crapper et al., 1976, *Brain*, 99:67-80) and one case report has documented markedly elevated levels of manganese in the tissues of a patient with Alzheimer's disease (Banta & Markesberg, 1977, *Neurology*, 27:213-216), which has led to the suggestion that high levels of these metals may be neurotoxic and lead to the development of Alzheimer's disease. It was interesting that the aluminum ions were found to be associated mainly with the nuclear chromatin in brain regions most likely to display neurofibrillary tangles in Alzheimer's disease. However, from a statistical point of view the absolute

differences found for the aluminum levels between normal and Alzheimer brains were far from convincing. It has recently been suggested that defects in the transcriptional splicing of mRNA coding for the tau complex of microtubule associated proteins occur (for review see Kosik, 1990, *Curr. Opinion Cell Biol.*, 2:101-104) and/or that inappropriate phosphorylation of these proteins exists (Grundke-Igbak et al., 1986, *Proc. Natl. Acad. Sci. USA*, 83:4913-4917; Wolozin & Davies, 1987, *Ann. Neurol.* 22:521-526; Hyman et al., 1988, *Ann. Neurol.*, 23:371-379; Bancher et al., 1989, *Brain Res.*, 477:90-99). Furthermore, reduction in the enzymes involved in the synthesis of acetylcholine has led to the view of Alzheimer's disease as a cholinergic system failure (Danes & Moloney, 1976, *Lancet*, ii:1403-14). However, even if cholinergic neurons are most at risk in Alzheimer's disease, it appears likely that these reductions in enzyme activity are secondary to the degenerative process itself rather than causally related.

2.1 THE DIAGNOSIS OF ALZHEIMER'S DISEASE

The diagnosis of Alzheimer's disease at autopsy is somewhat time-consuming but is definitive. The gross pathological changes are found in the brain, which is underweight, and shows generalized atrophy of both the gray and white matter of the cerebral cortex, particularly in the temporal and frontal lobes, with widening of the sulci and narrowing of the gyri as well as compensatory symmetrical dilation of the third and lateral ventricles (Adams & Victor, 1977, *Principles of Neurology*, pp. 401-407; Merritt, 1979, *A Textbook of Neurology*, 6th edition, Lea & Febiger, Philadelphia, pp. 484-489). The histological changes in the brain are definitive. The most common lesion is the neurofibrillary tangle (Kidd, 1963, *Nature*, 197:192-193; Kidd, 1964, *Brain* 87:307-320), which

consists of a tangled mass of paired helical filaments and occasional straight filaments located in the cytoplasm of affected neurons (Oyanagei, 1979, *Adv. Neurol. Sci.*, 18:77-88 (in Japanese) as quoted by 5 Grundke-Iqbali et al., 1985, *Acta Neuropathol.*, 66:52-61). The other characteristic histological lesions are Hirano bodies within nerve cells of certain brain regions, neuritic dystrophy and amyloid angiopathy. In addition, there are prominent argentophilic senile 10 neuritic plaques composed of enlarged, degenerating axonal endings, containing degraded cellular organelles and some paired helical filaments, that surround a core of mainly extracellular amyloid (Merritt, 1979, *A Textbook of Neurology*, 6th edition, 15 Lea & Febiger, Philadelphia, pp. 484-489). Small amounts of these histological changes are found also in the brains of almost all very old humans at autopsy, even if they showed no symptoms of Alzheimer's disease before death (Tomlinson & 20 Henderson, 1976, *Neurobiology of Aging*, p. 183, Terry & Gershon (eds.), Raven, New York; Ball, 1976, *Neuropathol. Appl. Neurobiol.*, 2:395; Ball, 1977, *Acta Neuropathol.*, 37:111-118). However, the number and total amount of these histological changes in brain 25 has been found to correlate well with the severity of the clinical signs and symptoms of Alzheimer's disease (Kidd, 1963, *Nature*, 197:192-193; Terry et al., 1964, *Am. J. Pathol.*, 44:269-297; Roth et al., 1966, *Nature*, 209:109-110; Blessed et al., 1968, *Br. J. Psychiat.*, 30 30 114:797-881; Tomlinson et al., 1970, *J. Neurol. Sci.*, 11:205-242; Wisniewski, 1976, *J. Neurol. Sci.*, 27:173-181).

The diagnosis of Alzheimer's disease during life is more difficult than at autopsy since it 35 depends upon an inexact clinical evaluation. In the middle stages and particularly in the earlier stages of the disease, the diagnosis is a matter of clinical

judgement and success is markedly dependent upon the experience and clinical acumen of the attending physician or consultant. In the late stages of the disease however, clinical diagnosis is relatively straight-forward even if it is not completely unequivocal. In all cases, a wide variety of other diseases, presenting at least partially overlapping clinical pictures, must be positively ruled out before a diagnosis of Alzheimer's disease can be made.

Usually a patient must be evaluated on a number of occasions over some period of time in order to document the deterioration in intellectual ability and other signs and symptoms before a diagnosis can be attempted with reasonable confidence. The necessity of repeated evaluation by a professional medical practitioner before a firm diagnosis can be made is costly, generates anxiety and can be frustrating to patients and their families. Furthermore, the development of an appropriate therapeutic strategy is greatly hampered by these difficulties in the objective and rapid diagnosis of the disease, particularly in the early stages where even a simple arrest of the progress of the disease would leave the patient with significant intellectual capacity and a reasonable quality of life.

No unequivocal laboratory test specific for Alzheimer's disease has been reported. European patent application No. 391714 discloses a method for the diagnosis of Alzheimer's disease based upon the detection of mature β -amyloid protein, its precursor protein or a fragment of β -amyloid protein in non-neuronal tissue biopsy using immunoassay techniques. However, this approach is non-specific since it has been recognized that a wide variety of degenerative diseases, lead to the production and deposition of β -amyloid protein in almost all human tissues. Furthermore, even though the gene coding for both the

β -amyloid protein (Golgaber et al., 1987, *Science*, 235:877-80; Tanzi et al., 1987a, *Science*, 235:880-884) and the gene for familial Alzheimer's disease (St. George-Hyslop et al., 1987, *Science*, 235:885-890) have been located on human chromosome 21, it has been shown that the linkage between the two genes is not very close (Van Broekhoven et al., 1987, *Nature*, 329:153-155; Tanzi et al., 1987b, *Nature*, 329:156-157). In addition, it is known that despite some earlier claims, β -amyloid protein forms no part of the paired helical filaments within neurofibrillary tangles (for review see Wischik et al., 1989, *Curr. Opinion Cell Biol.*, 1:115-122). Therefore, even though β -amyloid protein is deposited in many tissues of patients with Alzheimer's disease, it has not been definitively linked to Alzheimer's disease in a manner different to its association with many other degenerative diseases. Thus, the diagnostic usefulness of antibodies directed to mature β -amyloid protein, its precursor or any of its fragments must be considered marginal at best.

2.2 NEUROFIBRILLARY TANGLES AND ALZHEIMER'S DISEASE

It is now known that the only definitive feature of Alzheimer's disease is the presence of grossly increased quantities of neurofibrillary tangles within the affected cortical regions of brain compared to either normal brain from humans of any age or to brain from any disease state other than Alzheimer's disease itself. However, the neurofibrillary tangles have not heretofore been exploited for use in a diagnostic or screening assay for Alzheimer's disease.

The progression of Alzheimer's disease is characterized by a loss of cortical substance in the brain. This fact has been well documented over many years by many different researchers. The most

characteristic lesion in Alzheimer's disease is the presence of paired helical filaments in discrete, randomly interwoven groups or neurofibrillary tangles within affected cortical neurons. In addition, the 5 number and size of these tangles within an affected neuron as well as the total number of tangles and the total amount of constituent tau-protein in an affected brain correlates with the progression and severity of the disease. Therefore, it is believed that as these 10 tangles increase in size and number they must interfere with the physiological function of each cell in which they occur, eventually leading directly to the death and lysis of that cell. Recently, it has been reported that the cytosolic ATP-dependent 15 protease signal protein, ubiquitin, becomes attached to neurofibrillary tangles (Mori et al., 1987, *Science*, 235:1641-1644). Since ubiquitinated proteins are rapidly degraded, this suggests that the affected cell recognizes the tangles as a foreign structure 20 requiring degradation. It is further believed that this mechanism of cortical neuron death is responsible for the progressive loss of cortical substance and, therefore, the loss of intellectual capacity as well as the appearance of the other signs and symptoms of 25 Alzheimer's disease.

The paired helical filaments are composed of an unknown protein of 90,000 molecular weight (Mr) associated with various tau-protein species. A tightly bound helical core is formed between the 30 90,000 Mr protein and the large middle domain of the tau-protein as well as a region of the C-terminal domain, which contains the imperfect tandem repeat. The structural conformation of the helical core allows the N-terminal and C-terminal domains of the tau- 35 protein to protrude at some angle from the axis of the paired helical filament thereby forming a protease-sensitive coat around the paired helical filaments

(Wischik et al., 1988, *Proc. Natl. Acad. Sci. USA.*, 85:4884-4888). The research groups working in this area are directing their efforts towards characterizing the protease-resistant core of the 5 paired helical filaments in order to understand the nature of the stable interaction and the nature of the modification that occurs to tau-proteins in Alzheimer's disease (for reviews, see Wischik et al., 1989, *Curr. Opinion Cell Biol.*, 1:115-122; Kosik, 10 1990, *Curr. Opinion Cell Biol.*, 2:101-104). This orientation of research effort as well as research directed towards the molecular genetics of the tau-protein are likely to lead to an understanding of the primary cause of Alzheimer's disease.

15 From the foregoing, it is clear that no one concerned with Alzheimer's disease has realized that its diagnosis ultimately must depend upon the detection and quantitative measurement of the amount of the component substance or substances that 20 constitute these neurofibrillary tangles in victims of the disease. The detection of associated substances that can also be found in other disease states can never be as definitive as the detection of the actual substance building up in affected neurons in 25 Alzheimer's disease causing the eventual death of those cells. What has also not been realized is that the protease stability of the core of the paired helical filaments makes it unlikely that any part of the tau-protein or the 90,000 Mr protein present in 30 this stable core will ever be found outside the brain. The slow destruction of these stable cores, following their release by dead neurons, can be conceived to occur only *in situ* and as a consequence of 35 phagocytosis by microglia. The most likely reason for the reluctance or failure to recognize the potential of using components of the neurofibrillary tangles in the diagnosis of Alzheimer's disease relates to the

natural abhorrence that a person would feel if required to biopsy the brain of any living human being even in the last stages of the disease in order to measure these substances. The biopsy procedure is 5 extremely invasive and must leave the person so biopsied less than whole. However, the scientific community has not considered the possibility that biopsy might not be necessary in order to detect the substance or substances in question.

10 In contrast to the relevant literature, the diagnostic approach of the present invention is based on the recognition that the whole of the 200 amino acid N-terminal residues of the various tau-proteins as well as some portion of their 50 amino acid most C- 15 terminal residues will be released when cleaved from the filaments by ubiquitin-recognizing proteases or other proteases during degeneration and rupture of affected neurons. The diagnostic assays of the invention are based on the principle that it is these 20 cleaved latter segments of tau-proteins that can find their way into body fluids outside the brain and whose detection and quantitation are important for diagnostic purposes. Additional support for this last conclusion comes from the observation that other 25 brain-specific, soluble and protease-sensitive proteins find their way into blood and spinal fluid following head trauma (Phillips et al., 1980, Br. Med. J., 281:777-779; Brayne et al., 1982, Lancet, ii:1308- 9) and various other types of neurological disorders 30 (Thompson et al., 1980, J. Neurol. Sci., 47:241-254; Willson et al., 1980, Ann. Clin. Biochem., 17:110- 113).

3. SUMMARY OF THE INVENTION

35 The present invention relates to methods and kits for diagnosing, subtyping and monitoring Alzheimer's disease. The invention is based, in part,

on the discovery that proteolytic fragments of the amino and carboxy terminal amino acid residues of tau-proteins are released from the neurofibrillary tangles associated with the disease and can be detected in body fluids outside the brain.

- 5 The generation and purification of tau-proteins and peptide fragments of the amino terminal and carboxy terminal regions of tau-proteins are described. These tau-proteins and fragments thereof
10 may be used to generate monoclonal antibodies, polyclonal antibodies or Fab fragments that, in turn, can be used in immunoassays to detect circulating tau-peptides in suspected individuals. Alternatively, the tau-peptides themselves may be used in immunoassays to
15 detect circulating autoantibodies in such individuals.

3.1 DEFINITIONS

- The term tau-protein is defined herein as any one of the proteins that comprise a single 20 constituent part of the tau-complex of proteins.
- The tau-complex of proteins is defined as that group of microtubule associated proteins (MAPS) from vertebrate brain that have the following characteristics: (a) co-purify with tubulin during the 25 cycle purification of microtubules, particularly in the absence of glycerol (Asnes & Wilson, 1979, Anal. Biochem., 98:64-73; Murphy & Hiebsch, 1979, Anal. Biochem., 96:225-235); (b) separate from tubulin present in the microtubules obtained by the cycle 30 technique when an ice-cold sample of such a preparation is chromatographed on a phosphocellulose column, using 2-(N-morpholino)-ethanesulphonic acid (MES) buffer to remove tubulin and using MES buffer containing 1 M NaCl to remove the tau-complex of 35 proteins (Weingarten et al., 1975, Proc. Natl. Acad. Sci. USA, 72:1858-1862; Cleveland et al., 1977, J. Mol. Biol., 116:207-225; Cleveland et al., 1979, J.

Biol. Chem., 254:12670-12678); (c) are included in a column of Sepharose 6B when chromatographed on such a matrix and where they migrate as an aggregated species not far from the exclusion volume but have individual 5 unaggregated native molecular masses between 10,000 and 100,000 Mr regardless of axial ratio (Cleveland et al., 1977, J. Mol. Biol., 116:207-225); (d) react with any of a number of antibodies described in the literature as "anti-tau" or with a commercial antibody 10 described as anti-tau; (e) contain within each and every one of their C-terminal domains an imperfect tandem repeat of the type described in the literature (Lewis et al., 1988, Science, 242:936-939; Goedert et al., 1989, EMBO J., 8:393-399; Kanai et al., 1989, J. 15 Cell Biol., 109:1173-1184); and (f) are either heat-stable or heat-labile as described by Cleveland et al., 1977, J. Mol. Biol., 116:207-225.

The term "forward sandwich assay" is defined in its most basic form as an assay wherein the sample 20 to be tested containing the tau-peptide reacts with an anti-tau-peptide antibody that has been immobilized upon a solid substrate; then a labeled second anti-tau-peptide antibody is added, which reacts with the tau-peptide at a different site.

The term "reverse sandwich assay" is defined 25 in its most basic form as an assay wherein the labeled anti-tau-peptide antibody and sample to be tested containing the tau-peptide are first incubated together and then added to a second unlabeled anti- 30 tau-peptide antibody that had previously been immobilized upon a solid substrate as in the "forward sandwich assay". Both the labeled and the unlabeled anti-tau-peptide must react with the tau-peptide at a different site.

4. DESCRIPTION OF THE FIGURE

Figure 1 shows the complete nucleotide and amino acid sequences of one form of human tau-protein, reproduced from Goedert et al., 1988, Proc. Natl.

5 Acad. Sci. USA, 85:4051-4055.

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention results from the unexpected discovery of several physiological functions for individual proteins in the tau-complex of proteins that have not heretofore been described and are in addition to the well recognized function of promoting the polymerization of microtubules and/or their stability. This discovery has permitted the development of assays for the individual proteins in the tau-complex of proteins and their subsequent purification with retention of their native configuration and physiological activity. The invention is based, in part, on the discovery that in patients suffering from Alzheimer's disease there is proteolytic fragmentation of the tau-complex of proteins which occurs independently of phosphorylation, such that only the N-terminal domain comprising up to not more than the 200 most N-terminal amino acids or less and the C-terminal domain comprising up to only the 50 most C-terminal amino acids or less of tau will be released from the paired helical filaments, resident in the neurofibrillary tangle or free in the cytoplasm of affected neurons, and make their way into spinal fluid and blood.

This invention provides the first demonstration that any part of the tau-proteins of brain in victims of Alzheimer's disease are also present in body fluids outside the brain itself in concentrations greatly exceeding that found in normal humans that are not victims of Alzheimer's disease. This is achieved by examining a sample of body fluid,

preferably blood or spinal fluid, and detecting the presence and quantity of any of the tau-proteins or fragments thereof. The detection and quantitative measurement of any of these tau-proteins or fragments thereof in body fluids in accordance with this invention is useful in confirming a clinical diagnosis of Alzheimer's disease in affected patients and in following the course of the disease. The invention is also useful in monitoring the disease during and subsequent to a period of treatment with agents that are being tested for their ability to stabilize, decrease or prevent the release of tau-proteins or fragments thereof from the brain.

Alternatively, the invention is directed to the production of tau-peptides for use in detecting circulating anti-tau-peptide autoantibodies in body fluids outside the brain in victims of Alzheimer's disease. The detection of circulating anti-tau-peptide autoantibodies in accordance with this invention is useful in confirming a clinical diagnosis of Alzheimers disease in affected patients and in following the course of the disease.

For purposes of description only, the invention will be described in terms of: (a) generating tau-peptides; (b) generating antibodies that define the tau-peptide; and (c) diagnostic assays and kits for diagnosing subtyping or monitoring Alzheimer's disease.

30

5.1 PRODUCTION OF TAU-PEPTIDES

5.1.1 ENZYMATIC CLEAVAGE OF PURIFIED TAU-PROTEINS

The production of tau-peptides may be accomplished by isolating the paired helical filaments from human brains of patients who died with Alzheimers disease and purifying the helical complex containing the tau-protein and the 90,000 Mr protein (see Section 6, *infra*). The tau-protein is associated with the

90,000 Mr protein such that the 200 most amino terminal residues and the 50 most carboxy terminal residues protrude from the helical core of the complex thereby rendering those fragments susceptible to 5 proteolytic enzymes.

The cleavage of the tau-protein into two large fragments of amino acid residues 1 to 151 and 154 to 352 and the dipeptide, Ser-Arg, may be accomplished using either one of the arginine-specific 10 proteolytic enzymes such as thrombin (EC 3.4.13) as described recently (Joly et al., 1989, *J. Cell Biol.*, 109:2289-2294) or clostridiopeptidase B (clostripain) (EC 3.4.4.20). The preferred embodiment uses clostripain because the enzyme is a sulphydryl enzyme, 15 requiring calcium ions for full activity. Consequently, its activity can be terminated conveniently by the addition of excess iodoacetamide and ethylene glycol-bis(β -aminoethyl ether) N,N,N',N'-tetraacetic acid (EGTA). In the case of either 20 protease the concentration of tau-protein is adjusted to 100 μ g/ml before beginning the digestion. Purified clostripain is used at a concentration of 4 international units/ml in the following buffer (50 mM phosphate buffer pH 7.7, 1 mM β -mercaptoethanol, and 1 25 mM calcium acetate). Soybean trypsin inhibitor (clostripain/inhibitor molar ratio = 10/1) is added in order to eliminate any small residual trypsin activity in commercially available preparations of the enzyme. The cleavage reaction is conducted at 37°C and is 30 terminated by the addition of a sufficient volume of a 100 mM stock solution EGTA, pH 7.7, containing 100 mM iodoacetimide to give a final concentration of 2 mM EGTA in the protease reaction mixture. The exact time required for proteolysis varies with each tau-protein 35 and markedly depends upon the batch of clostripain used. Therefore, the optimum time for a single cleavage must be determined for each combination of

clostripain batch and tau-protein used. The time course of the cleavage reaction is determined by conducting the reaction as described above, but on a 20 μ l volume and assaying the cleavage reaction by 5 subjecting samples at various times to sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS PAGE) according to the method of Laemmli, (*Nature*, 1970, 227:680-684) as modified by Studier, *Sci.*, 176:367-376 (1972) using a 10% (w/v) polyacrylamide resolving gel 10 followed by Serva blue staining and destaining in the usual manner of anyone familiar with the art.

The two large tau-peptide fragments resulting from either thrombin or clostripain proteolysis may be further cleaved by digestion with 15 trypsin, which cleaves on the carboxy terminus of lysine or arginine residues. See for example, the techniques described in *Current Protocols in Molecular Biology*, Ausubel et al., Green Publish. Assoc. & Wiley Interscience, Ch. 10.

20 The sequence of tau-peptides derived from proteolytic digestion may be identified using the Edman degradation method of protein sequencing. This method sequentially removes one amino acid residue at a time from the amino terminal end of a peptide for 25 subsequent sequence identification by chromatographic procedures. See for example, the techniques described in Konigsberg and Steinman, 1977, *Strategy and Methods of Sequence Analysis*, in Neurath and Hill (eds.), *The Proteins* (3rd ed.) Vol. 3, pp. 1-178, Academic Press. 30 In addition, sequence analysis of tau-peptides may be accelerated by using an automated liquid phase amino acid sequenator following recently described techniques (Hewick et al., 1981, *J. Biol. Chem.*, 256:7990-7997; Stein and Udefriend, 1984, *Analy. Chem.*, 136:7-23), thereby allowing for the analysis of 35 picomolar quantities of tau-peptides containing up to 50 amino acid residues in length.

5.1.2 CHEMICAL SYNTHESIS OF TAU-PEPTIDES

Tau-peptides can also be produced by chemical synthesis of the amino acid sequence of a tau-protein (Goedert et al., 1988, *Proc. Natl. Acad. Sci. USA*, 85:4051-4055), as predicted from the cloning and sequencing of a cDNA coding for a tau-protein. This tau-protein sequence information may be utilized to predict the appropriate amino and carboxy terminal tau-peptides to be chemically synthesized using standard peptide synthesis methods known in the art. These methods include a solid-phase method devised by R. Bruce Merrifield, (Erickson and Merrifield, "Solid-Phase Peptide Synthesis"; in *The Proteins*, Volume 2, H. Neurath & R. Hill (eds.) Academic Press, I: York pp. 255-257; Merrifield, 1986, "Solid phase synthesis", *Science*, 242:341-347). In the solid phase method, amino acids are added stepwise to a peptide chain that is linked to an insoluble support such as polystyrene beads. A major advantage of this method is that the desired product at each step is bound to beads that can be rapidly filtered and thus the need to purify intermediates is obviated. All of the reactions are carried out in a single vessel, which eliminates losses due to repeated transfers of products. This solid phase method of chemical peptide synthesis can readily be automated making it feasible to routinely synthesize peptides containing about 50 residues in good yield and purity (Stewart and Young, 1984, *Solid Phase Peptide Synthesis*, 2nd ed., Pierce Chemical Co.; Tam et al., 1983, *J. Am. Chem. Soc.*, 105:6442). For example, tau-peptides corresponding to amino acid residues 1 to 30 and 331 to 352 as depicted in Figure 1 could be synthesized.

5.1.3 CLONING AND EXPRESSION OF RECOMBINANT TAU-PROTEINS AND/OR TAU-PEPTIDES

The production of tau-peptides can further be achieved by recombinant DNA technology. For example, appropriate tau nucleotide coding sequences may be synthesized, cloned and expressed in appropriate host cells. Since the DNA sequence encoding for a tau-protein is known (Goeddert et al., 1988, Proc. Natl. Acad. Sci., USA 85:4051-4055), DNA probes may be synthesized by standard methods known in the art to screen cDNA libraries prepared from brain tissue of Alzheimer's disease patients for the specific tau-protein cDNA's. These DNA probes can further be used to isolate the entire family of tau-protein genes from these cDNA libraries using methods which are well known to those skilled in the art. See, for example, the techniques described in Maniatis et al., 1982, *Molecular Cloning A Laboratory Manual*, Cold Spring Harbor Laboratory, N.Y., Chapter 7.

The polymerase chain reaction (PCR) technique can be utilized to amplify the individual members of the tau family for subsequent cloning and expression of tau-protein cDNAs (e.g., see U.S. patent numbers 4,683,202; 4,683,195; 4,889,818; Gyllensten et al., 1988, Proc. Nat'l Acad. Sci. USA, 85:7652-7656; Ochman et al., 1988, Genetics, 120:621-623; Triglia et al., 1988, Nucl. Acids. Res., 16:8156; Frohman et al., 1988, Proc. Nat'l Acad. Sci. USA, 85:8998-9002; Loh et al., 1989, Science, 243:217-220).

Methods which are well known to those skilled in the art can be used to construct expression vectors containing tau-proteins or fragments thereof coding sequences and appropriate transcriptional/translational control signals. These methods include in vitro recombinant DNA techniques, synthetic techniques and in vivo recombination/genetic recombination. See, for example, the techniques

described in Maniatis et al., 1982, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., Chapter 12.

- A variety of host-expression vector systems
- 5 may be utilized to express tau-proteins or fragments thereof. These include but are not limited to microorganisms such as bacteria transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing a coding sequence
- 10 for a tau-protein or fragment thereof; yeast transformed with recombinant yeast expression vectors containing a coding sequence for a tau-protein or fragment thereof; insect cell systems infected with recombinant virus expression vectors (e.g.,
- 15 baculovirus) containing a coding sequence for a tau-protein or fragment thereof; or animal cell systems infected with recombinant virus expression vectors (e.g., adenovirus, vaccinia virus) containing a coding sequence for a tau-protein or fragment thereof.
- 20 The expression elements of these vectors vary in their strength and specificities. Depending on the host/vector system utilized, any of a number of suitable transcription and translation elements, including constitutive and inducible promoters, may be
- 25 used in the expression vector. For example, when cloning in bacterial systems, inducible promoters such as pL of bacteriophage λ, plac, ptrp, ptac (ptrp-lac hybrid promoter) and the like may be used; when cloning in insect cell systems, promoters such as the
- 30 baculovirus polyhedrin promoter may be used; when cloning in mammalian cell systems, promoters such as the adenovirus late promoter or the vaccinia virus 7.5K promoter may be used. Promoters produced by recombinant DNA or synthetic techniques may also be
- 35 used to provide for transcription of the inserted coding sequence for a tau-protein or fragment thereof.

In yeast, a number of vectors containing constitutive or inducible promoters may be used. For a review see, Current Protocols in Molecular Biology, Vol. 2, 1988, Ed. Ausubel et al., Greene Publish.

5 Assoc. & Wiley Interscience Ch. 13; Grant et al., 1987, Expression and Secretion Vectors for Yeast, in Methods in Enzymology, Eds. Wu & Grossman, 1987, Acad. Press, N.Y., Vol. 153, pp. 516-544; Glover, 1986, DNA Cloning, Vol. II, IRL Press, Wash., D.C. Ch.3; and

10 Bitter, 1987, Heterologous Gene Expression in Yeast, Methods in Enzymology, Eds. Berger & Kimmel, Acad. Press, N.Y., Vol. 152, pp. 673-684; and The Molecular Biology of the Yeast *Saccharomyces*, 1982, Eds. Strathern et al., Cold Spring Harbor Press, Vols. I

15 and II. For complementation assays in yeast, cDNAs for tau-proteins or fragments thereof may be cloned into yeast episomal plasmids (YEP) which replicate autonomously in yeast due to the presence of the yeast 2μ circle. The tau-protein or fragment thereof sequence may be cloned behind either a constitutive yeast promoter such as ADH or LEU2 or an inducible promoter such as GAL (Cloning in Yeast, Chpt. 3, R. Rothstein In; DNA Cloning Vol. II, A Practical Approach, Ed. DM Glover, 1986, IRL Press, Wash.,

20 25 D.C.). Constructs may contain the 5' and 3' non-translated regions of a cognate tau-protein mRNA or those corresponding to a yeast gene. YEp plasmids transform at high efficiency and the plasmids are extremely stable. Alternatively vectors may be used

30 35 which promote integration of foreign DNA sequences into the yeast chromosome.

A particularly good expression system which could be used to express tau-proteins or fragments thereof is an insect system. In one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The

tau-protein or fragment thereof coding sequence may be cloned into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of the polyhedrin gene results in production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (e.g., see Smith et al., 1983, *J. Biol.*, 46:586; Smith, U.S. Patent No. 4,215,051).

In cases where an adenovirus is used as an expression vector, the tau-protein or fragment thereof coding sequence may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vivo* or *in vitro* recombination.

Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the tau-protein of fragment thereof in infected hosts. (e.g., See Logan & Shenk, 1984, *Proc. Natl. Acad. Sci.*, (USA) 81:3655-3659). Alternatively, the vaccinia 7.5K promoter may be used. (e.g., see Mackett et al., 1982, *Proc. Natl. Acad. Sci.*, (USA) 79:7415-7419; Mackett et al., 1984, *J. Virol.*, 49:857-864; Panicali et al., 1982, *Proc. Natl. Acad. Sci.*, 79:4927-4931).

Specific initiation signals may also be required for efficient translation of the inserted tau-protein or fragment thereof coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where the entire tau-protein genome, including its own initiation codon and adjacent sequences, are inserted into the appropriate

expression vectors, no additional translational control signals may be needed. However, in cases where only a portion of the tau-protein coding sequence is inserted, exogenous translational control signals, including the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the tau-protein or fragment thereof coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bitter et al., 1987, *Methods in Enzymol.*, 153:516-544).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression driven by certain promoters can be elevated in the presence of certain inducers, (e.g., zinc and cadmium ions for metallothionein promoters). Therefore, expression of the genetically engineered tau-protein or fragment thereof may be controlled. This is important if the protein product of the cloned foreign gene is lethal to host cells. Furthermore, modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed.

The host cells which contain the tau-protein or fragment thereof coding sequence and which express the biologically active tau-protein or fragment

thereof gene product may be identified by at least four general approaches: (a) DNA-DNA hybridization; (b) the presence or absence of "marker" gene functions; (c) assessing the level of transcription as measured by expression of tau-protein mRNA transcripts in host cells; and (d) detection of tau-protein gene products as measured by immunoassays or by its biological activity.

In the first approach, the presence of the tau-protein or fragment thereof coding sequence inserted in the expression vector can be detected by DNA-DNA hybridization using probes comprising nucleotide sequences that are homologous to the tau-protein coding sequence or particular portions thereof substantially as described recently (Goedert et al., 1988, Proc. Natl. Acad. Sci. USA, 85:4051-4055).

In the second approach, the recombinant expression vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (e.g., thymidine kinase activity, resistance to antibiotics, resistance to methotrexate, transformation phenotype, occlusion body formation in baculovirus, etc.). For example, if the tau-protein or fragment thereof coding sequence is inserted within a marker gene sequence of the vector, recombinants containing the tau-protein or fragment thereof coding sequence can be identified by the absence of the marker gene function. Alternatively, a marker gene can be placed in tandem with the tau-protein or fragment thereof coding sequence under the control of the same or different promoter used to control the expression of the tau coding sequence. Expression of the marker in response to induction or selection indicates expression of the tau-protein coding sequence.

In the third approach, transcriptional activity for the tau-protein or fragment thereof

coding region can be assessed by hybridization assays. For example, RNA can be isolated and analyzed by Northern blot using a probe homologous to the tau-protein or fragment thereof coding sequence or 5 particular portions thereof substantially as described (Goedert et al., 1988, Proc. Natl. Acad. Sci. USA, 85:4051-4055). Alternatively, total nucleic acids of the host cell may be extracted and assayed for hybridization to such probes.

10 In the fourth approach, the expression of the tau-protein or fragment thereof product can be assessed immunologically, for example by Western blots, immunoassays such as radioimmunoprecipitation, enzyme-linked immunoassays and the like.

15 Once a recombinant that expresses a tau-protein or fragment thereof is identified, the gene product should be analyzed. This can be achieved by assays based on the physical, immunological or functional properties of the product.

20 A tau-protein or fragment thereof should be immunoreactive whether it results from the expression of the entire gene sequence, a portion of the gene sequence or from two or more gene sequences which are ligated to direct the production of chimeric proteins.

25 This reactivity may be demonstrated by standard immunological techniques, such as radioimmunoprecipitation, radioimmune competition, or immunoblots.

30

5.2 GENERATION OF ANTIBODIES THAT DEFINE TAU-PEPTIDES

Various procedures known in the art may be used for the production of antibodies to epitopes of the tau-protein. Such antibodies include but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments and an Fab expression library. 35 For the production of antibodies, various host animals

may be immunized by injection with a particular tau-protein, or a synthetic tau-peptide, including but not limited to rabbits, mice, rats, etc. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *corynebacterium parvum*.

Monoclonal antibodies to peptides of tau may be prepared by using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include but are not limited to the hybridoma technique originally described by Kohler and Milstein, (*Nature*, 1975, 256:495-497), the more recent human B-cell hybridoma technique (Kosbor et al., 1983, *Immunology Today*, 4:72) and the EBV-hybridoma technique (Cole et al., 1985, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention monoclonal antibodies specific to tau-peptides may be produced in germ-free animals utilizing recent technology (PCT/US90/02545). According to the invention, human antibodies may be used and can be obtained by using human hybridomas (Cote et al., 1983, *Proc. Natl. Acad. Sci.*, 80:2026-2030) or by transforming human B cells with EBV virus *in vitro* (Cole et al., 1985, in, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, pp. 77-96). In fact, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, *Proc. Natl. Acad. Sci.*, 81:6851-6855; Neuberger et al., 1984, *Nature*, 312:604-608; Takeda et al., 1985, *Nature*, 314:452-454) by splicing the genes

sample to be tested is brought into contact with the bound molecule. After a suitable period of incubation, for a period of time sufficient to allow formation of an antibody-antigen binary complex, a 5 second antibody, labelled with a reporter molecule capable of inducing a detectable signal, is then added and incubation is continued allowing sufficient time for binding with the antigen at a different site and the formation of a ternary complex of antibody- 10 antigen-labeled antibody. Any unreacted material is washed away, and the presence of the antigen is determined by observation of a signal, which may be quantitated by comparison with a control sample containing known amounts of antigen. Variations on 15 the forward sandwich assay include the simultaneous assay, in which both sample and antibody are added simultaneously to the bound antibody, or a reverse sandwich assay in which the labelled antibody and sample to be tested are first combined, incubated and 20 added to the unlabelled surface bound antibody. These techniques are well known to those skilled in the art, and the possibility of minor variations will be readily apparent. As used herein, "sandwich assay" is intended to encompass all variations on the basic two- 25 site technique.

For the sandwich assays of the present invention, the only limiting factor is that both antibodies have different binding specificities for the tau-peptide. Thus, a number of possible 30 combinations are possible.

As a more specific example, in a typical forward sandwich assay, a primary antibody is either covalently or passively bound to a solid support. The solid surface is usually glass or a polymer, the most 35 commonly used polymers being cellulose, polyacrylamide, nylon, polystyrene, polyvinylchloride or polypropylene. The solid supports may be in the

form of tubes, beads, discs or microplates, or any other surfaces suitable for conducting an immunoassay. The binding processes are well known in the art.

Following binding, the solid phase-antibody complex is 5 washed in preparation for the test sample. An aliquot of the body fluid containing the tau-peptide to be tested is then added to the solid phase complex and incubated at 25°C for a period of time sufficient to allow binding of any tau-peptide present to the antibody specific for tau-peptide. The second 10 antibody is then added to the solid phase complex and incubated at 25°C for an additional period of time sufficient to allow the second antibody to bind to the primary antibody-antigen solid phase complex. The 15 second antibody is linked to a reporter molecule, the visible signal of which is used to indicate the binding of the second antibody to any antigen in the sample. By "reporter molecule", as used in the present specification is meant a molecule which by its 20 chemical nature, provides an analytically detectable signal which allows the detection of antigen-bound antibody. Detection must be at least relatively quantifiable, to allow determination of the amount of antigen in the sample, this may be calculated in 25 absolute terms, or may be done in comparison with a standard (or series of standards) containing a known normal level of antigen.

The most commonly used reporter molecules in this type of assay are either enzymes or fluorophores.

30 In the case of an enzyme immunoassay an enzyme is conjugated to the second antibody, often by means of glutaraldehyde or periodate. As will be readily recognized, however, a wide variety of different conjugation techniques exist, which are well known to 35 the skilled artisan. Commonly used enzymes include horseradish peroxidase, glucose oxidase, β -galactosidase and alkaline phosphatase, among others.

The substrates to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by the corresponding enzyme, of a detectable color change. For example, p-nitrophenyl phosphate is suitable for use with alkaline phosphatase conjugates; for peroxidase conjugates, 1,2-phenylenediamine or toluidine are commonly used. It is also possible to employ fluorogenic substrates, which yield a fluorescent product rather than the chromogenic substrates noted above. In all cases, the enzyme-labelled antibody is added to the first antibody-tau-peptide complex and allowed to bind to the complex, then the excess reagent is washed away. A solution containing the appropriate substrate is then added to the tertiary complex of antibody-antigen-labelled antibody. The substrate reacts with the enzyme linked to the second antibody, giving a qualitative visual signal, which may be further quantitated, usually spectrophotometrically, to give an evaluation of the amount of antigen which is present in the serum sample.

Alternately, fluorescent compounds, such as fluorescein or rhodamine, may be chemically coupled to antibodies without altering their binding capacity. When activated by illumination with light of a particular wavelength, the fluorochrome-labelled antibody absorbs the light energy, inducing a state of excitability in the molecule, followed by emission of the light at a characteristic longer wavelength. The emission appears as a characteristic color visually detectable with a light microscope. As in the enzyme immunoassay (EIA), the fluorescent-labelled antibody is allowed to bind to the first antibody-tau-peptide complex. After washing the unbound reagent, the remaining ternary complex is then exposed to light of the appropriate wavelength, and the fluorescence observed indicates the presence of the antigen.

Immunofluorescence and EIA techniques are both very well established in the art and are particularly preferred for the present method. However, other reporter molecules, such as radioisotopes, 5 chemiluminescent or bioluminescent molecules may also be employed. It will be readily apparent to the skilled artisan how to vary the procedure to suit the required use.

Alternatively, the sample to be tested 10 either human blood or spinal fluid containing the tau-peptide may be used in a single site immunoassay wherein it is adhered to a solid substrate either covalently or noncovalently. An unlabeled anti-tau-peptide antibody is brought into contact with the 15 sample bound on the solid substrate. After a suitable period of incubation, for a period of time sufficient to allow formation of an antibody-antigen binary complex a second antibody, labelled with a reporter molecule capable of inducing a detectable signal, is 20 then added and incubation is continued allowing sufficient time for the formation of a ternary complex of antigen-antibody-labeled antibody. For the single site immunassay, the second antibody may be a general antibody (i.e., xenogeneic antibody to immunoglobulin, 25 particularly anti-(IgM and IgG) linked to a reporter molecule) that is capable of binding an antibody that is specific for the tau-peptide of interest.

Alternatively, the purified tau-proteins or fragments thereof, described in Section 5.1, *supra*, 30 may be used in a diagnostic assay to detect circulating anti-tau-peptide autoantibodies wherein they are adhered to a solid support either covalently or non-covalently. The sample, either human blood or spinal fluid diluted in an appropriately buffered 35 medium, is added to the solid support and a sufficient time is allowed for complex formation between the tau-proteins or fragments thereof and any cognate

autoantibodies in the sample. The supernatant is removed and the solid support is washed to remove any non-specifically bound proteins. To the complex may be added xenogeneic antisera to human immunoglobulin, particularly anti-(human Ig M and Ig G) in an appropriately buffered medium. The xenogeneic antisera will normally be labeled with a reporter molecule as described above for the forward sandwich assay. Instead of xenogeneic antisera, proteins specific for the immune complex may be employed, e.g., *S. aureus* protein A. The label may then be detected as described above for the forward sandwich assay.

6. EXAMPLE: PRODUCTION AND PURIFICATION OF IMMUNOGENS FOR ANTIBODY PRODUCTION

6.1. PURIFICATION OF MICROTUBULES FROM BOVINE BRAIN BY THE CYCLE PROCEDURE AS A SOURCE OF NATIVE, PHYSIOLOGICALLY ACTIVE MICROTUBULE ASSOCIATED PROTEINS

The cycle purification of microtubules from bovine brain was performed in the presence of guanosine triphosphate and low concentrations of magnesium ions in order to obtain high ratios of microtubule associated proteins to tubulin. This cycle-purification was carried out in five separate steps according to a modification of the method described by Asnes & Wilson, (1979, *Anal. Biochem.*, 98:64-73).

Step (1) Transport & Dissection: Eight bovine brains (approximately 350 gram (g) each) were removed, cut into pieces, placed in ice-cold transport buffer [20 mM phosphoric acid (adjusted to pH 6.75 with 2M NaOH) 100 mM sodium glutamate, 300 mM sucrose] containing ice cubes made from transport buffer and transported in an ice bucket from the abattoir to the laboratory. The meninges, superficial blood vessels and the majority of the white matter was removed and

discarded. The remaining brain tissue (approximately 1200 g) was drained and weighed.

Step (2) Homogenization: The selected brain tissue was dispersed using two separate maneuvers sequentially. The weighed brain tissue from step (1) was passed once through a domestic electric mincer and added to homogenization buffer [200 mM phosphoric acid (adjusted to pH 6.75 with 2 M NaOH), 100 mM sodium glutamate, 300 mM sucrose, 4 mM β -mercaptoethanol, 0.3 mM phenylmethanesulphonylfluoride (PMSF) (stock solution, 100 mM in dimethylformamide (DMF)), 0.3 mM $\text{Na-p-tosyl-1-lysine chloromethylketone}$ (TLCK) (prepared in PMSF stock solution), 50 $\mu\text{g/ml}$ leupeptin, few crystals of catalase] (at 0°C and at a concentration of 1.5 ml buffer / g tissue). The material was dispersed by gentle stirring with a glass rod. The resulting suspension was then homogenized in three batches with two complete strokes (up and down twice for each batch separately) of a motor driven 1 liter (L) glass (2.2 inch diameter x 18 inch long) Potter - Elvehjem homogenizer fitted with a 2 inch long teflon pestle (0.005 inch clearance) at 0°C.

Step (3) First Cycle: Approximately 3000 ml of the homogenate was added to twelve 250 ml plastic centrifuge tubes and centrifuged at 27,880 g (13,000 rpm in two Sorval RC5B preparative centrifuges containing two GSA rotors precooled to 3°C) for 53 minutes at 0-4°C. The supernatants were carefully removed, combined and cofactor buffer [2.5 mM GTP, .50 mM MgCl₂, 1.0 mM EGTA (10 x stock solution adjusted to pH 6.75 at 0°C with NaOH)] prepared in homogenization buffer was added. The solution was mixed and then approximately 1L portions together with a glass thermometer was placed in separate polyethene sleeves (10 inch x 14 inch) and heat sealed. The loaded sleeves were gently agitated in a 50°C water bath until the temperature of their contents reached 30°C

whereupon they were immediately transferred to a 30°C water bath where the incubation continued without further agitation for the remainder of a total period of 30 minutes. Assembly was followed viscometrically
5 using calibrated 100-size Cannon Ubbelohde glass viscometers. Approximately 2400 ml of the assembled extract was transferred to 12 clean 250 ml plastic centrifuge jars and centrifuged at 27,880 g (13,000 rpm in two Sorval RC5B preparative centrifuges
10 containing two Sorval GSA rotors prewarmed to 30°C) for 42 minutes at 30°C. The supernatant was carefully removed with an aspirator and its volume was measured, recorded and discarded.

Step (4) Second Cycle: The final pellet from
15 the first cycle was resuspended in ice-cold homogenization buffer without sucrose (10% of volume of the supernatant from the first cycle) using a precooled small Dounce homogenizer. Approximately 220 ml of the resuspended pellet was incubated at 0°C
20 for 30 minutes, added to six 36 ml plastic centrifuge tubes, and centrifuged at 39,000 g (14,627 rpm in a Sorval OTD centrifuge containing a Sorval AH-627 rotor precooled to 3°C) for 40 minutes at 0 to 4°C. The supernatant was carefully transferred to a 1L glass
25 conical flask and cofactor buffer was added. The solution was mixed and gently swirled in the 50°C water bath until the temperature reached 30°C. The flask was then immediately transferred to a 30°C water bath where the incubation continued without further
30 agitation for a total period of only 10 minutes. The extract was transferred to six 36 ml plastic centrifuge tubes and centrifuged at 39,000 g (14,726 rpm in a Sorval OTD ultracentrifuge containing a Sorval AH-627 rotor) for 30 minutes at 30°C. The
35 supernatant was removed carefully with an aspirator and its volume was measured and discarded.

Step (5) Third Cycle - The final pellet from the second cycle was resuspended in ice-cold homogenization buffer without sucrose (40% of the volume of the supernatant from the second cycle) using a clean precooled small Dounce homogenizer.

5 Approximately 90 ml of resuspended pellet was incubated at 0°C for 30 minutes, transferred to three 36 ml tubes, and centrifuged at 39,000 g (14,726 rpm in a Sorval OTD ultracentrifuge containing a Sorval AH-627 rotor with 36 ml buckets) for 40 minutes at 0 to 4°C. Approximately 80 ml of supernatant was carefully transferred to a 500 ml glass conical flask and cofactor buffer was added. The solution was mixed and gently swirled in the 50°C water bath until the 10 temperature of the contents of the flask reached 30°C. Then the flask was immediately transferred to the 30°C water bath where the incubation continued without further agitation for a total period of 20 minutes. The warm extract was transferred to six 17 ml plastic 15 centrifuge tubes and centrifuged at 39,000 g (Sorval PTD centrifuge containing a Sorval AH-627 rotor with 17 ml buckets) for 40 minutes at 30°C. The supernatant was removed carefully with an aspirator and discarded. Each tube contained a pellet of 20 approximately 140 mg of microtubule (MT) proteins (approximately 50% tubulin and 50% MAPS) and was 25 centrifuged at 39,000 g (Sorval PTD centrifuge containing a Sorval AH-627 rotor with 17 ml buckets) for 40 minutes at 30°C. The supernatant was removed carefully with an aspirator and discarded. Each tube contained a pellet of approximately 140 mg of microtubule (MT) proteins (approximately 50% tubulin and 50% MAPS) and was stored at -70°C.

30 6.2. ISOLATION OF THE TAU CLASS OF
MICROTUBULE ASSOCIATED PROTEINS
FROM CYCLE PURIFIED MICROTUBULES

The total MAPS fraction of cycle purified microtubules was separated from tubulin by a modification of the method of Weingarten, (1975, Proc. Natl. Acad. Sci. USA, 72:1858-1862). A pellet of 35 microtubules from the cycle purification method was resuspended using a small Dounce homogenizer in MES

buffer (0.1 M MES; 1 mM EGTA; 0.5 mM MgCl₂ and 1 mM β -mercaptoethanol) so that the resulting solution had an absorbance at 280 nm of 2.0 - 2.5 and then depolymerized by incubation for 30 min at 0°C. The 5 resulting solution was centrifuged at 100,000 g for 1 hour and the pellet discarded. The supernatant was filtered through a 0.2 μ milipore filter and applied to a phosphocellulose column (1.1 cm diameter x 2.6 cm length, 2.5 ml bed volume) that had previously been 10 equilibrated in MES buffer. Tubulin was eluted with MES buffer in the void volume of the column and when the absorbance of the eluate had returned to the baseline value, the total MAPS fraction was eluted (either 0.1 or 0.2 ml fractions) with MES buffer 15 containing 1.0 M NaCl and collected as a single complex peak of UV-absorbing material that contained multiple proteins.

The total MAPS fraction eluted from the phosphocellulose column was immediately desalting using 20 the rapid Sephadex G-25 centrifugation method of Penefsky (*J. Biol. Chem.*, 1977, 252:2891-2899). The desalting total MAPS fraction was stirred at 0° C and solid ammonium sulphate added until its concentration reached 35% (w/v). The stirring was continued for 30 25 minutes and then the suspension was centrifuged at 20,000 g for 15 minutes. The supernatant was removed and again stirred at 0° C and more solid ammonium sulphate added until its concentration reached 45% (w/v). After a further 15 minute stirring the 30 suspension was again centrifuged at 20,000 g for 15 minutes and the supernatant discarded. The pellet from this last centrifugation step was dissolved in Mes buffer and applied to a column of hydroxyapatite (1 cm dia x 10 cm length) and eluted with Mes buffer. 35 The fractions containing only four closely spaced peptides of apparent Mr 45,000 to 65,000 by SDS-PAGE were combined. This total eluted tau fraction was

- 36 -

reduced to a volume of 1.0 ml with a sartorius
collodion membrane operated in water under reduced
pressure, according to the instructions of the
manufacturer, and then divided into 0.1 ml portions in
5 0.5 ml plastic minifuge tubes and stored at -20°C.

The invention is not limited to the
embodiments described herein and may be modified or
varied without departing from the scope of the
invention.

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WHAT IS CLAIMED IS:

1. A method for diagnosing, subtyping or monitoring Alzheimer's disease in a patient, comprising assaying a sample of body fluid obtained from the patient for the presence of a tau-peptide using either an anti-tau-peptide antibody or an anti-tau-peptide Fab fragment, wherein further the tau-peptide is derived from proteolytic action on neurofibrillary tangles resulting in fragments from the amino terminal 200 amino acids or carboxy terminal 50 amino acids.
2. A method for diagnosing, subtyping or monitoring Alzheimer's disease in a patient, comprising assaying a sample of body fluid obtained from the patient for the presence of an anti-tau-peptide autoantibody.
3. The method for diagnosing, subtyping or monitoring Alzheimer's disease according to claims 1 or 2, wherein the assay is a radioimmunoassay, an enzyme-linked immunosorbant assay, a sandwich assay, a precipitin reaction, a gel immunodiffusion assay, an agglutination assay, a fluorescent immunoassay, a protein A immunoassay or an immunoelectrophoresis assay.
4. A kit for detecting the presence of a tau-peptide in a sample of body fluid comprising an anti-tau-peptide antibody or an anti-tau-peptide Fab fragment and means for detecting the binding of the tau-peptide with the antibody or fragment.
5. A kit for detecting the presence of an anti-tau-peptide autoantibody in a sample of body fluid

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comprising a tau-peptide and means for detecting the binding of the autoantibody with the tau-peptide.

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37 CGCCCTCTGCACTATAGGTGAACTTGAACCAAGG

1 Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr
 1 ATG GCT GAG CCC CGC CAG TTC GAA GTG ACG TAC GGG AGC TAC GGT AAA GAT CAC GCT GGG ACG TAC GGG TTG GGC AGC AAA GAT CAG GGG GGC TAC ACC

31 Met His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro Ser Leu Glu Asp Glu Ala
 31 ATG CAC CAA GAC CAA GAG GGT GAC ACC GAC GCT GGC CTG AAA GCT GAA GAA GCA GCA GGC ATT GGA GAC ACC CCC AGC CTG GAA GAC GAA CCT

61 Ala Gly His Val Thr Gln Ala Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Ala Lys Gly Ala Asp Gly Lys
 101 GCT GGT CAC GTG ACC CAA GCT GGT CGC ATG GTC AGT AAA AGC AAA GAC GGG ACT GGA AGC GAT GAC AAA AAC GCC AAG GGG GCT GAT GGT AAA

91 Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro Pro Ala
 271 ACG AAG ATC GCC ACA CCC CGG CGA GCA GGC CCT CCA GGC AAC GGC CAG GGC CAG AAC GGC ACC AGC ATT CCA GCA AAA ACC CCG CCC GCT 1/2

121 Pro Lys Thr Pro Pro Ser Gly Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
 361 CCA AAG ACA CCA CCC AGC TCT CCT GAA CCT CCA AAA TCA GGG GAT CGC AGC GGC TAC AGC AGC CCC GGC ACT CCC GGC AGC

151 Arg Ser Arg Thr Pro Ser Leu Pro Thr Arg Glu Pro Lys Val Ala Val Arg Thr Pro Pro Lys Ser Pro Ser Ser
 451 CGC TCC CGC ACC CCC TCC CTA ACC CCA CCC ACC CGG GAG CCC AAG AAG GTG GCA GTG GTC CGT ACT CCA CCC AAG TCG CCG TCT TCC

181 Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His
 541 GCC AAG AGC CGC CTG CAG ACA GCC CCC GTG CCC ATG CCA GAC CTG AAG AAT GTC AAG TCC AAG ATC GGC TCC ACT GAG AAC CTG AAG CAC

SUBSTITUTE SHEET

FIG. 1

211 Gln Pro Gly Gly Lys Val Glu Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His
 631 CAG CCC GGA GGC GGG AAG GTG CAA ATA GTC TAC AAA CCA GTT GAC CTG AGC AAG GTG ACC TCC AAG TGT GGC TCA TTA GGC AAC ATC CAT
 241 His Lys Pro Gly Gly Glu Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser Lys Ile Gly Ser Leu Asp Asn
 721 CAT AAA CCA GGA GGT GGC CAG GTG GAA GTA AAA TCT GAG ATT GTC AAA GTC CAG TCG AAG ATT GGG TCC CTG GAC AAT
 271 Ile Thr His Val Pro Gly Gly Asn Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly
 811 ATC ACC CAC GTC CCT GCC GGA GAA AAT AAA AAG ATT GAA ACC CAC AAG CTG ACC TTC CGC GAG AAC GCC AAA GGC AAG ACA GAC CAC GGG
 301 Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser Ile Asp Met
 901 GCG GAG ATC GTG TAC AAG TCG CCA GTG GTG TCT GGG GAC ACG TCT CCA CGG CAT CTC AGC AAT GTC TCC ACC GGC AGC ATC GAC ATG
 331 Val Asp Ser Pro Gln Leu Ala Asp Glu Val Ser Ala Lys Gln Gly Leu ***
 991 GTA GAC TCG CCC CAG CTC GCC ACC CTA GCT GAG GTG TCT GCC TCC CTG GGC AAG CAG GGT TTG TGA TCAGGGCCCTGG

FIG. 1 (CONT.)

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) :Please See Extra Sheet.

US CL :435/7.92, 7, 808, 811; 436/ 518, 515, 516; 530/387.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/7.92, 7, 808, 811; 436/ 518, 515, 516; 530/387.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

CAS, MEDLINE, APS, DIALOG

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	PROCEEDINGS OF NATIONAL ACADEMY OF SCIENCES, USA, VOLUME 83, ISSUED JULY 1986, I. GRUNDKE-IQBAL ET AL., "ABNORMAL PHOSPHORYLATION OF THE MICROTUBULE-ASSOCIATED PROTEIN I (TAU) IN ALZHEIMER CYTOSKELETAL PATHOLOGY", PAGES 4913-4917, SEE ENTIRE DOCUMENT.	1-5
Y	JOURNAL OF NEUROSCIENCE RESEARCH, VOLUME 25, ISSUED 1990, H. KSIEZAK-REDING ET AL., "MAPPING OF THE ALZ-50 EPITOPE IN MICROTUBULE-ASSOCIATED PROTEINS TAU", PAGES 412-419, ENTIRE DOCUMENT.	1-5
Y	LANCET, ISSUED 06 JULY 1985, P. D. MEHTA ET AL., "PAIRED HELICAL FILAMENT ANTIGEN IN CSF", PAGE 35. SEE ENTIRE DOCUMENT.	1-5
Y	AMERICAN JOURNAL OF PATHOLOGY, VOLUME 126, NO. 1, ISSUED JANUARY 1987, SHU-HUI YEN ET AL., "ALZHEIMER'S NEUROFIBRILLARY TANGLES CONTAIN UNIQUE EPITOPE AND EPITOPE IN COMMON WITH THE HEAT-STABLE MICROTUBULE ASSOCIATED PROTEINS TAU AND MAP2", PAGES 81-91, ENTIRE DOCUMENT.	1-5

 Further documents are listed in the continuation of Box C. See patent family annex.

• Special categories of cited documents:			
"A"	document defining the general state of the art which is not considered to be part of particular relevance	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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Date of the actual completion of the international search

27 August 1992

Date of mailing of the international search report

10 SEP 1992

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INTERNATIONAL SEARCH REPORT

International application No.
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A. CLASSIFICATION OF SUBJECT MATTER:
IPC (5): G01N 33/53; A61K 35/12